FIG. 1

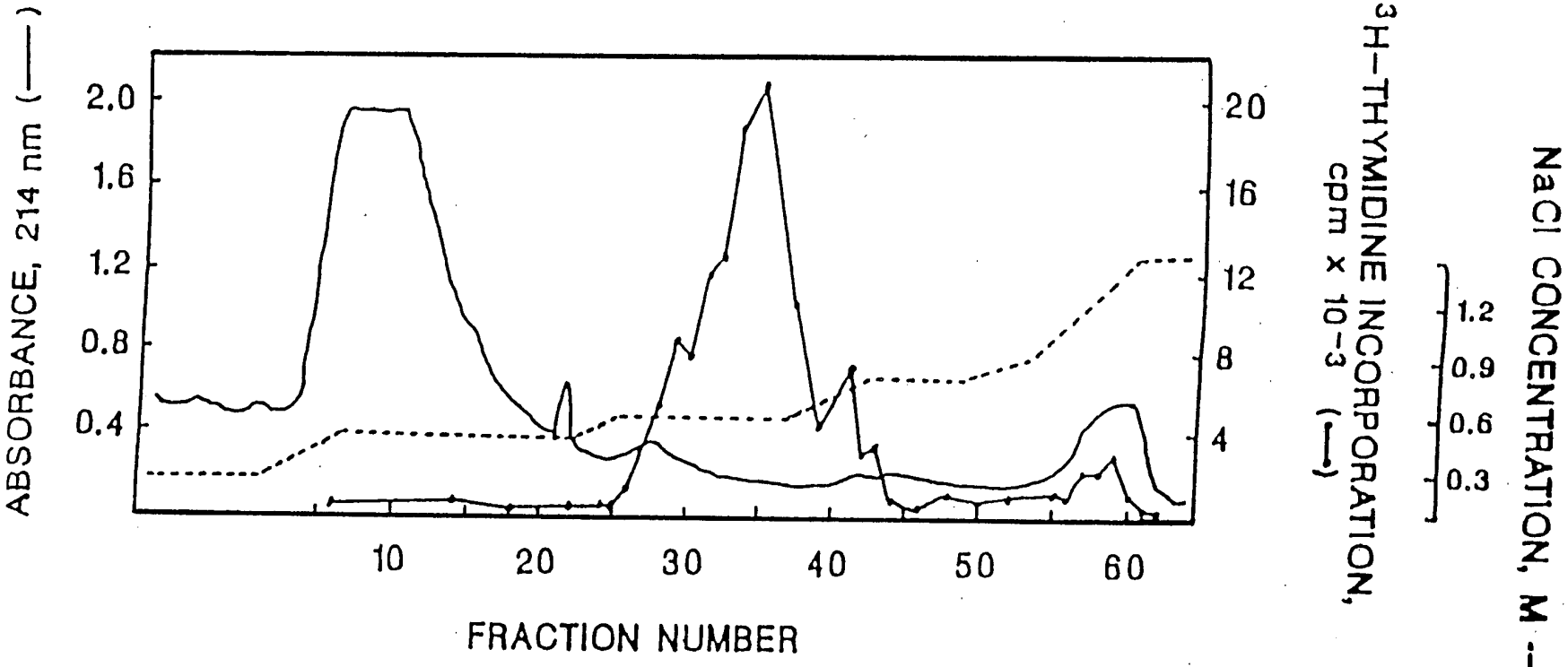

ABSORBANCE, 214 nm (——)
2.0
1.6
1.2
0.8
0.4
20
16
12
8
4
10
20
30
40
50
60
FRACTION NUMBER
^{3}H-THYMIDINE INCORPORATION, cpm x 10-3 (– –)
NaCl CONCENTRATION, M ----
1.2
0.9
0.6
0.3

FIG. 2A

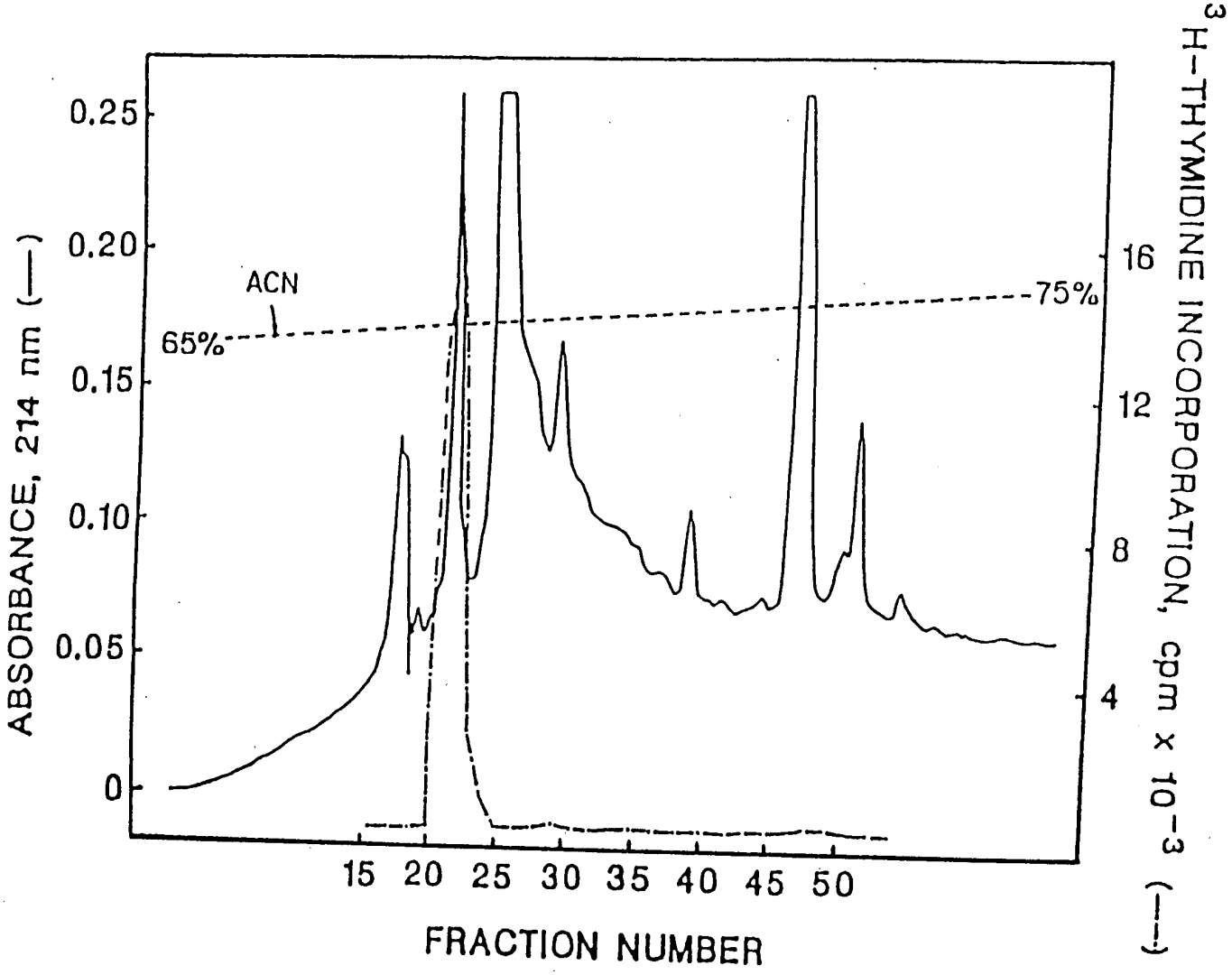

ABSORBANCE, 214 nm (—)
0.25
0.20
0.15
0.10
0.05
0
ACN
65%
75%
15 20 25 30 35 40 45 50
FRACTION NUMBER
^{3}H-THYMIDINE INCORPORATION, cpm x 10^{-3} (---)
16
12
8
4

FIG. 2C

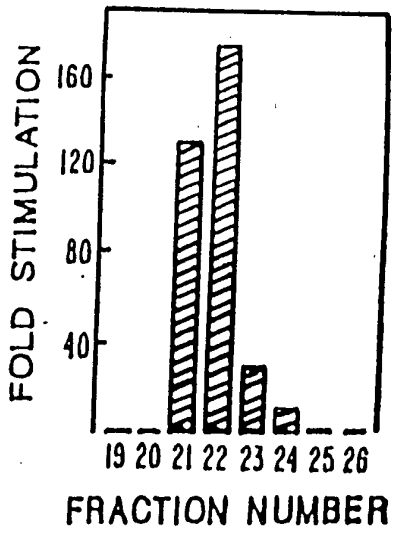

FOLD STIMULATION
160
120
80
40
19 20 21 22 23 24 25 26
FRACTION NUMBER

FIG. 2B

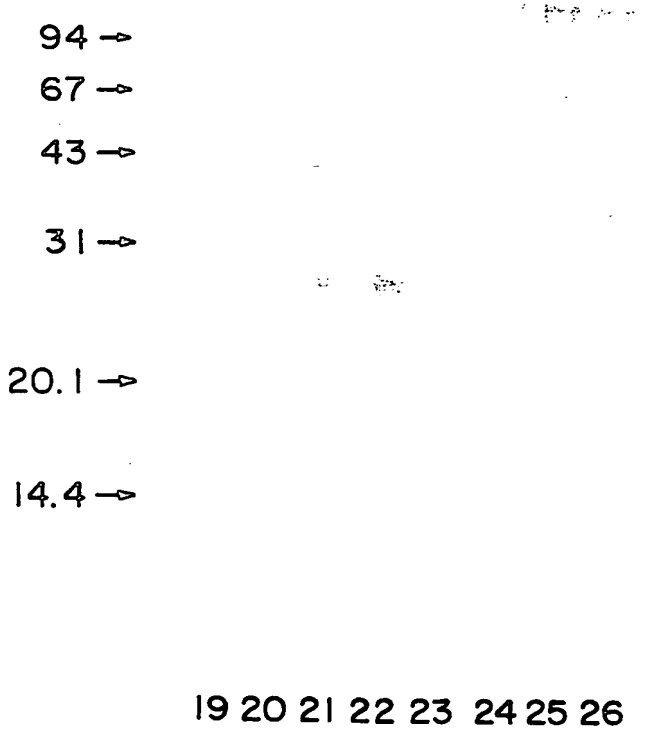


FIG. 3

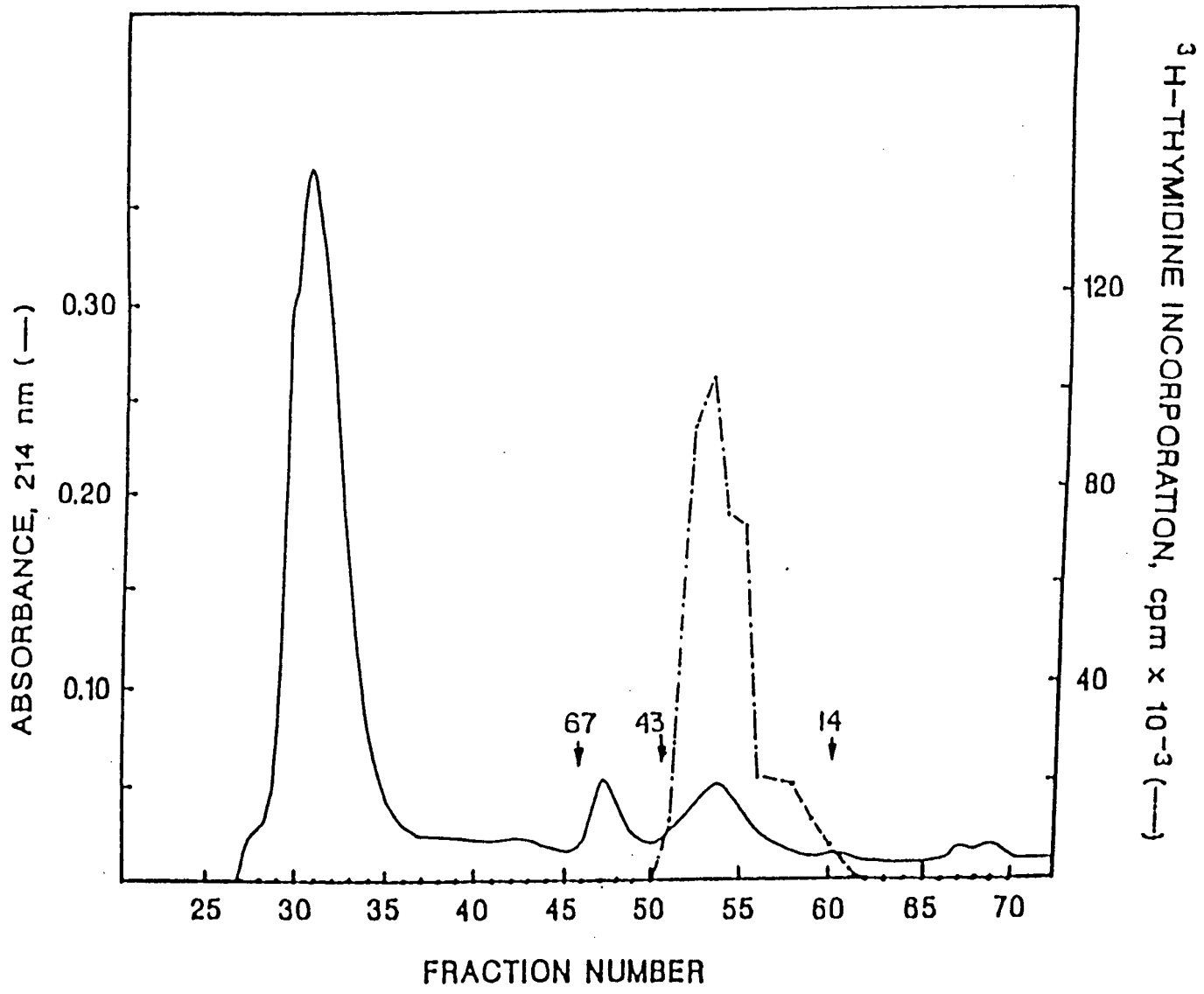

ABSORBANCE, 214 nm (—)
0.30
0.20
0.10
67
43
14
120
80
40
^{3}H-THYMIDINE INCORPORATION, cpm x 10^{-3} (—)
25
30
35
40
45
50
55
60
65
70
FRACTION NUMBER

FIG. 4

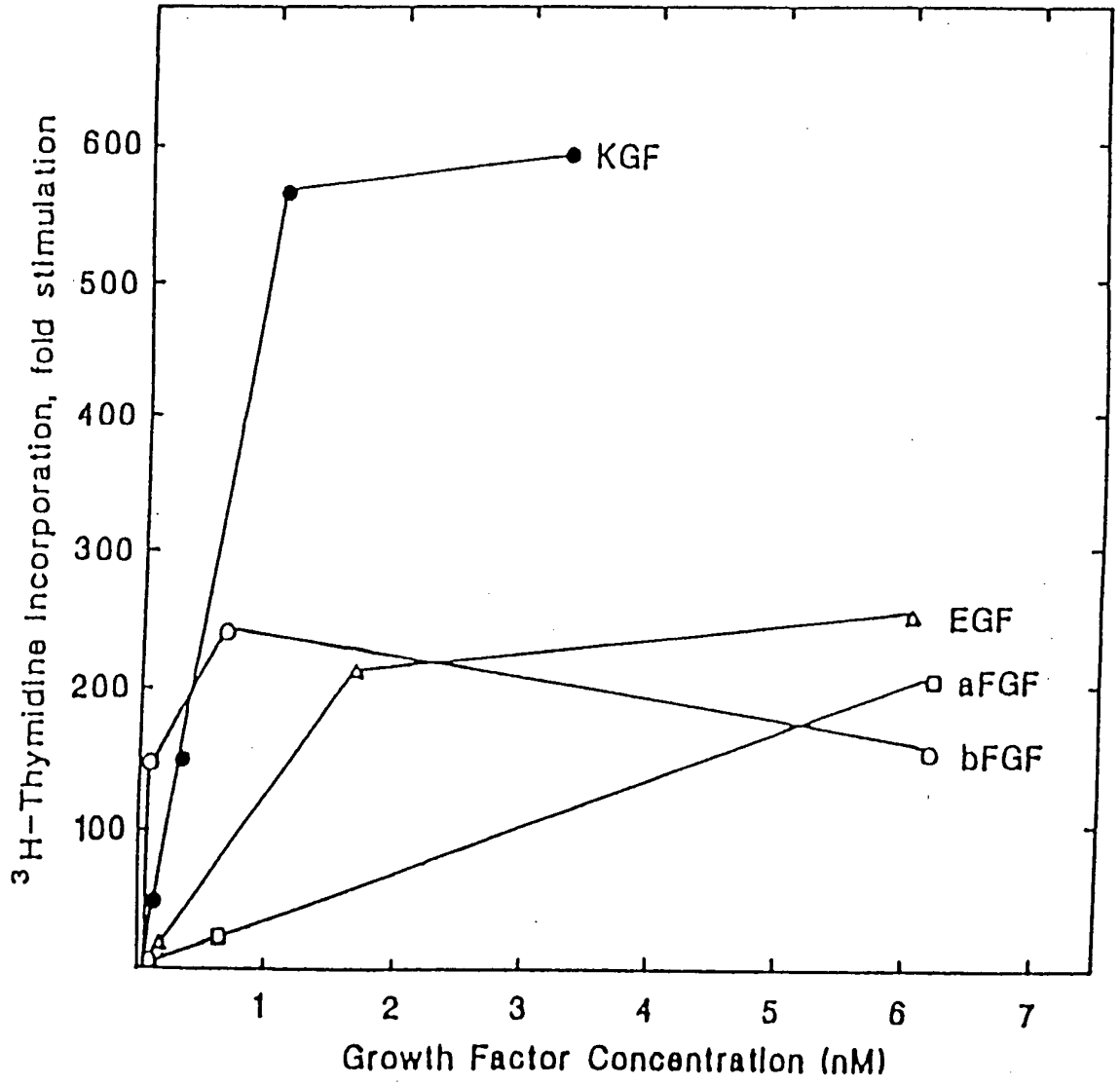

600
500
400
300
200
100
^{3}H-Thymidine Incorporation, fold stimulation
KGF
EGF
aFGF
bFGF
1
2
3
4
5
6
7
Growth Factor Concentration (nM)

FIG. 5(a) FIG. 5(b) FIG. 5(c) FIG. 5(d)

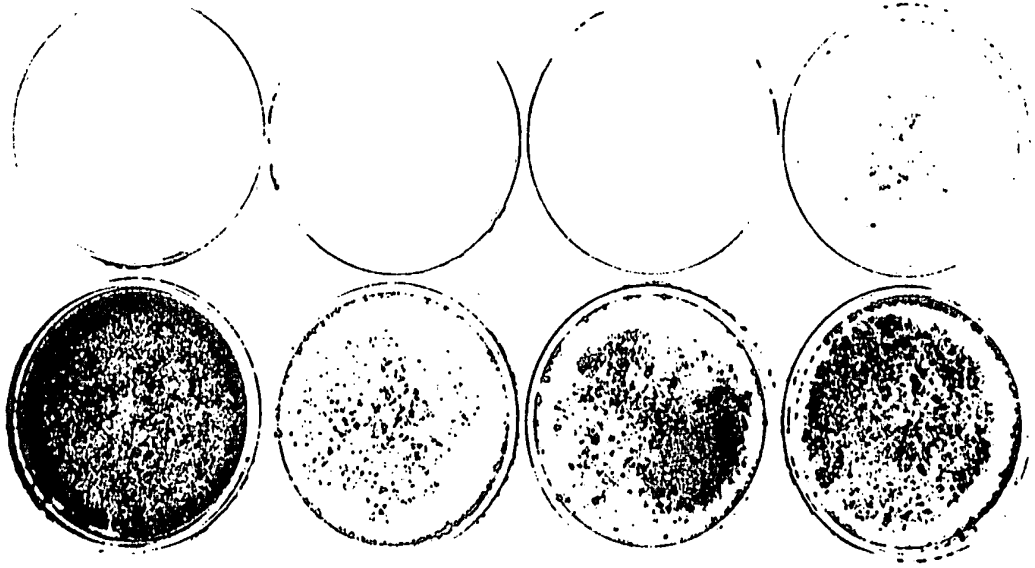


FIG. 5(e) FIG. 5(f) FIG. 5(g) FIG. 5(h)

FIG. 6

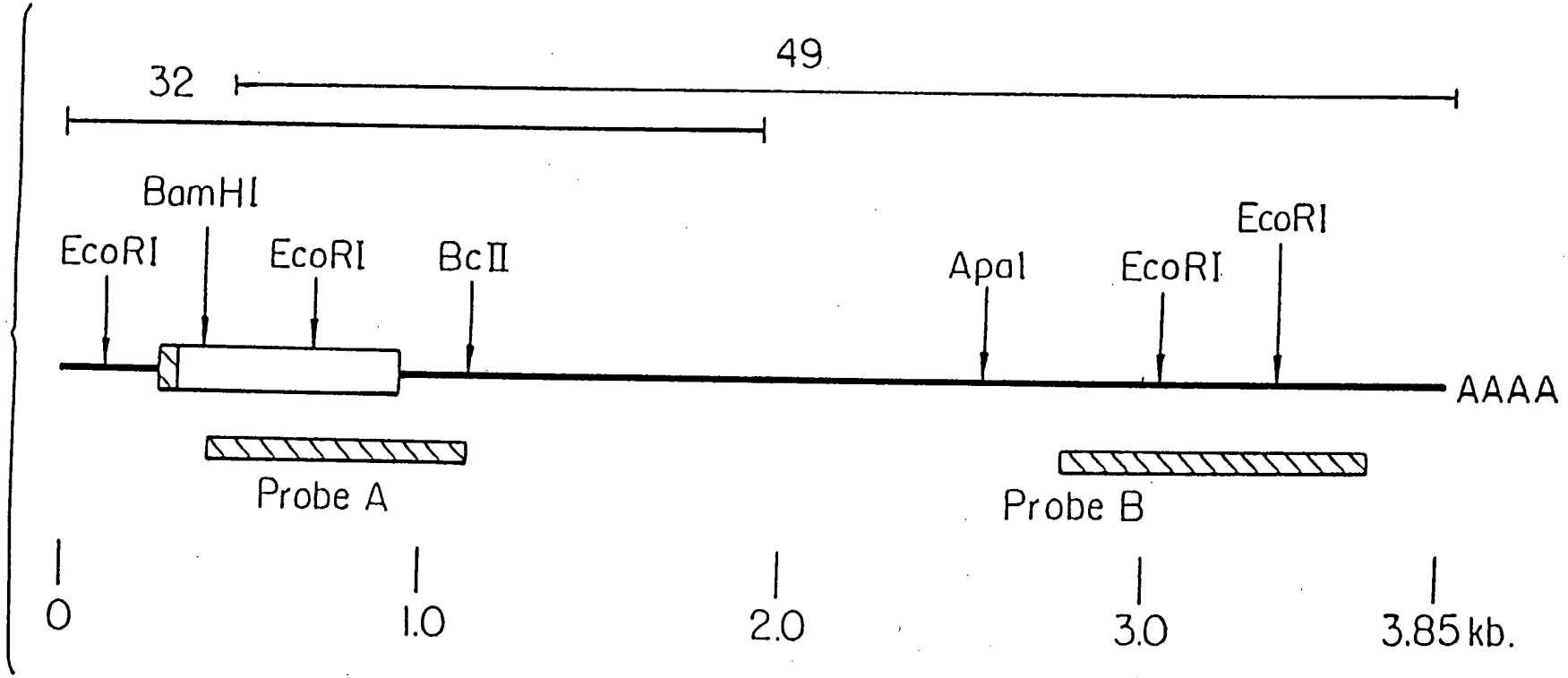

32
49
BamHI
EcoRI
EcoRI
BcII
ApaI
EcoRI
EcoRI
AAAA
Probe A
Probe B
0
1.0
2.0
3.0
3.85 kb.

FIG. 7A

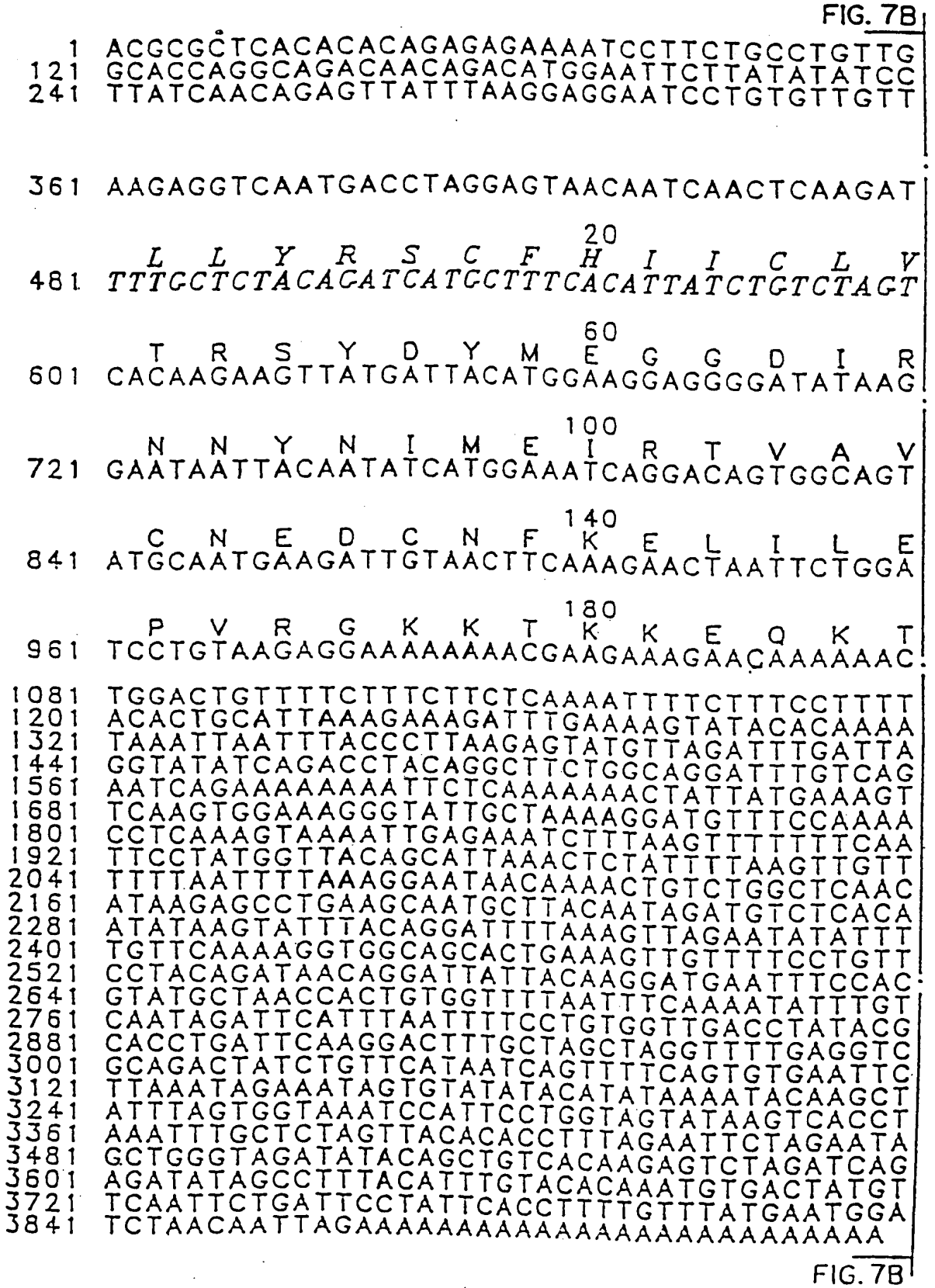


FIG. 7B
1 ACGCGCTCACACACAGAGAGAAAATCCTTCTGCCTGTTG
121 GCACCAGGCAGACAACAGACATGGAATTCTTATATATCC
241 TTATCAACAGAGTTATTTAAGGAGGAATCCTGTGTTGTT
361 AAGAGGTCAATGACCTAGGAGTAACAATCAACTCAAGAT
20
L L Y R S C F H I I C L V
481 TTTGCTCTACACATCATGCTTTCACATTATCTGTCTAGT
60
T R S Y D Y M E G G D I R
601 CACAAGAAGTTATGATTACATGGAAGGAGGGGATATAAG
100
N N Y N I M E I R T V A V
721 GAATAATTACAATATCATGGAAATCAGGACAGTGGCAGT
140
C N E D C N F K E L I L E
841 ATGCAATGAAGATTGTAACTTCAAAGAACTAATTCTGGA
180
P V R G K K T K K E Q K T
961 TCCTGTAAGAGGAAAAAAAACGAAGAAAGAACAAAAAAC
1081 TGGACTGTTTTCTTTCTTCTCAAAATTTTCTTTCCTTTT
1201 ACACTGCATTAAAGAAAGATTTGAAAAGTATACACAAAA
1321 TAAATTAATTTACCCTTAAGAGTATGTTAGATTTGATTA
1441 GGTATATCAGACCTACAGGCTTCTGGCAGGATTTGTCAG
1561 AATCAGAAAAAAAAATTCTCAAAAAAACTATTATGAAAGT
1681 TCAAGTGGAAAGGGTATTGCTAAAAGGATGTTTCCAAAA
1801 CCTCAAAGTAAAATTGAGAAATCTTTAAGTTTTTTTCAA
1921 TTCCTATGGTTACAGCATTAAACTCTATTTTAAGTTGTT
2041 TTTTAATTTTAAAGGAATAACAAAACTGTCTGGCTCAAC
2161 ATAAGAGCCTGAAGCAATGCTTACAATAGATGTCTCACA
2281 ATATAAGTATTTACAGGATTTTAAAGTTAGAATATATTT
2401 TGTTCAAAAGGTGGCAGCACTGAAAGTTGTTTTCCTGTT
2521 CCTACAGATAACAGGATTATTACAAGGATGAATTTCCAC
2641 GTATGCTAACCACTGTGGTTTTAATTTCAAAATATTTGT
2761 CAATAGATTCATTTAATTTTCCTGTGGTTGACCTATACG
2881 CACCTGATTCAAGGACTTTGCTAGCTAGGTTTTGAGGTC
3001 GCAGACTATCTGTTCATAATCAGTTTTCAGTGTGAATTC
3121 TTAAATAGAAATAGTGTATATACATATAAAATACAAGCT
3241 ATTTAGTGGTAAATCCATTCCTGGTAGTATAAGTCACCT
3361 AAATTTGCTCTAGTTACACACCTTTAGAATTCTAGAATA
3481 GCTGGGTAGATATACAGCTGTCACAAGAGTCTAGATCAG
3601 AGATATAGCCTTTACATTTGTACACAAATGTGACTATGT
3721 TCAATTCTGATTCCTATTCACCTTTTGTTTATGAATGGA
3841 TCTAACAATTAGAAAAAAAAAAAAAAAAAAAAAAAAAA
FIG. 7B

FIG. 7B

FIG. 7A

FIG. 7C

```
ATTTATGGAAACAATTATGATTCTGCTGGAGAACTTTT
AGCTGTTAGCAACAAAACAAAAGTCAAATAGCAAACAG
ATCAGGAACTAAAAGGATAAGGCTAACAATTTGGAAAG


TCATTTTCATTATGTTATTCATGAACACCCGGAGCACT
                    30
  G   T   I   S   L   A   C   N   D   M   T   P
GGGTACTATATCTTTAGCTTGCAATGACATGACTCCAG
                    70
  V   R   R   L   F   C   R   T   Q   W   Y   L
AGTGAGAAGACTCTTCTGTCGAACACAGTGGTACCTGA
                   110
  G   I   V   A   I   K   G   V   E   S   E   F
TGGAATTGTGGCAATCAAAGGGGTGGAAAGTGAATTCT
                   150
  N   H   Y   N   T   Y   A   S   A   K   W   T
AAACCATTACAACACATATGCATCAGCTAAATGGACAC
                   190
  A   H   F   L   P   M   A   I   T   *
AGCCCACTTTCTTCCTATGGCAATAACTTAATTGCATA

ATTTTTTAGTAATCAAGAAAGGCTGGAAAAACTACTGA
ATCAGATTTAGTAACTAAAGGTTGTAAAAAATTGTAAA
TCTGATAATGATTATTTAAATATTCCTATCTGCTTATA
ATAATCAAGCCACACTAACTATGGAAAATGAGCAGCAT
CAATAAAAATAGATAATTTAACAAAAGTACAGGATTAGA
ATCTTGTATATAAGATAGCAACAGTGATTGATGATAAT
GTAACATAATCTATCTTTGTATAATTCATATTTGGGAA
TTTGAACTTTATTGTTTTGTTATTTAAGTTTATGTTAT
GGCAAGTTTCCCTCCCTTTTCTGACTGACACTAAGTCT
CAGAACAATACAAATATGTAAAAACTCTTTCACCACAT
GAATGCATGGGTAGAAAATATCATATTTTAAAACTATG
AGATGGCAAGAGCACAATGCCCAAAATAGAAGATGCAG
TTCAAAAGTCTTTCATTGGCAGATCTTGGTAGCACTTT
CATTCAAGTCCCTTTACATAAATAGTATTTGGTAATAC
ACCAGGATGTAGAAAACTAGAAAGAACTGCCCTTCCTC
AGGCTTCAGTAACTGTAGTCTTGTGAGCATATTGAGGG
ACTGAATGTTTATAGACAAAAGAAAATACACACTAAAA
ATGTTAGGACCAAATGCTCTTTGTCTATGGAGTTATAC
AAAAAAGACTTCTAGAAATATGTACTTTAATTATTTGT
TTAAAACTGTAAGGGGCCTCCATCCCTCTTACTCATTT
TTAGCACATGCTTTCTACTCTTCGATTATTAGTATTAT
CTTGGCAATGCACTTCATACACAATGACTAATCTATAC
AAGCTTTGTGCAAAATATACATATAAGCAGAGTAAGCC
```

FIG. 7A

FIG. 7C

FIG. 7C

FIG. 7B

```
CAGCTGAGAAATAGTTTGTAGCTACAGTAGAAAGGCTCAAGTT
CGTCACAGCAACTGAACTTACTACGAACTGTTTTTATGAGGAT
AGCAAGTACTCTTTCTTAAATCAATCTACAATTCACAGATAGG

                M  H  K  W  I  L  T  W  I  L  P  T
                                              10
ACACTATAATGCACAAATGGATACTGACATGGATCCTGCCAAC

        40
E  Q  M  A  T  N  V  N  C  S  S  P  E  R  H
                                              50
AGCAAATGGCTACAAATGTGAACTGTTCCAGCCCTGAGCGACA

        80
R  I  D  K  R  G  K  V  K  G  T  Q  E  M  K
                                              90
GGATCGATAAAAGAGGCAAAGTAAAAGGGACCCAAGAGATGAA

      120
Y  L  A  M  N  K  E  G  K  L  Y  A  K  K  E
                                             130
ATCTTGCAATGAACAAGGAAGGAAAACTCTATGCAAAGAAAGA

      160
H  N  G  G  E  M  F  V  A  L  N  Q  K  G  I
                                             170
ACAACGGAGGGGAAATGTTTGTTGCCTTAAATCAAAAGGGGAT


TGGTATATAAAGAACCCAGTTCCAGCAGGGAGATTTCTTTAAG

AAAACTGATCAAGCTGGACTTGTGCATTTATGTTTGTTTTAAG
ACTGGTTGTACAATCATGATGTTAGTAACAGTAATTTTTTTCT
AAATGGCTGCTATAATAATAATAATACAGATGTTGTTATATAA
TTTAAAATGCTTTCTAGTGAAAAATTATAATCTACTTAAACTCT
ACATGCTTATACCTATAAATAAGAACAAAATTTCTAATGCTGC
ACTGTACTTCATCTTACTTGCCACAAAATAACATTTTATAAAT
TTATAAAAAAAAAAACCTTAATAAGCTGTATCTGTTTCATATGC
AGCACACAGCACTTGGGCCAGCAAATCCTGGAAGCAGACAAAA
ATTCTTGCCAATTAATTGGATCATATAAGTAAAATCATTACAA
TATATTTAAATTTAGTAATTTTCTAATCTCTAGAAATCTCTGC
TTAAGAATAAGGGGCCCTGAATGTCATGAAGGCTTGAGGTCAG
ATATGTTCACCAATGGGAGGTCAATATTTATCTAATTTAAAAG
ATTTATAGATGAGAGTTATATGAAAAGGCTAGGTCAACAAAAA
AGATATACTCTTGGGAGAGCATGAATGGTATTCTGAACTAT
CAGAGGAGGACTTAGTTTTTCATATGTGTTTCCTTAGTGCCTA
CTAATCTTCATTTTAAAAGGGTAAAACATGACTATACAGAAAT
TTCCATCAAATTACATAGCAATGCTGAATTAGGCAAAACCAAC
TTTTCTCCTATTTTTAAATTTATTATGCAAATTTTAGAAAATA
GTAGTCTAGGAAATTGAGATTTTGATACACCTAAGGTCACGCA
TAGCTAATGGTCTTTGGCATGTTTTTGTTTTTTATTTCTGTTG
TGTGATGATTTGACTCAAAAGGAGAAAAGAAATTATGTAGTTT
TTTTAAAAATGTTCTTTGAAAGATAAAATTAAATACATTGAGTT
```

FIG. 7B

FIG. 8

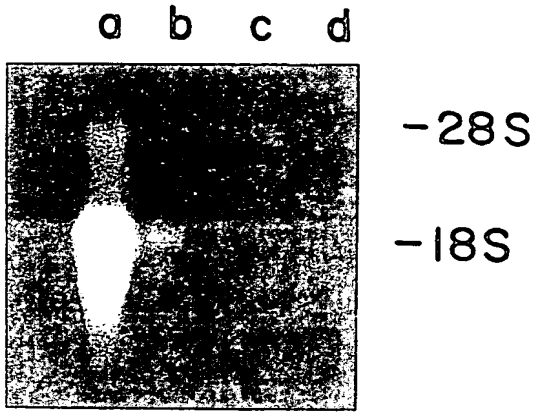


FIG. 9

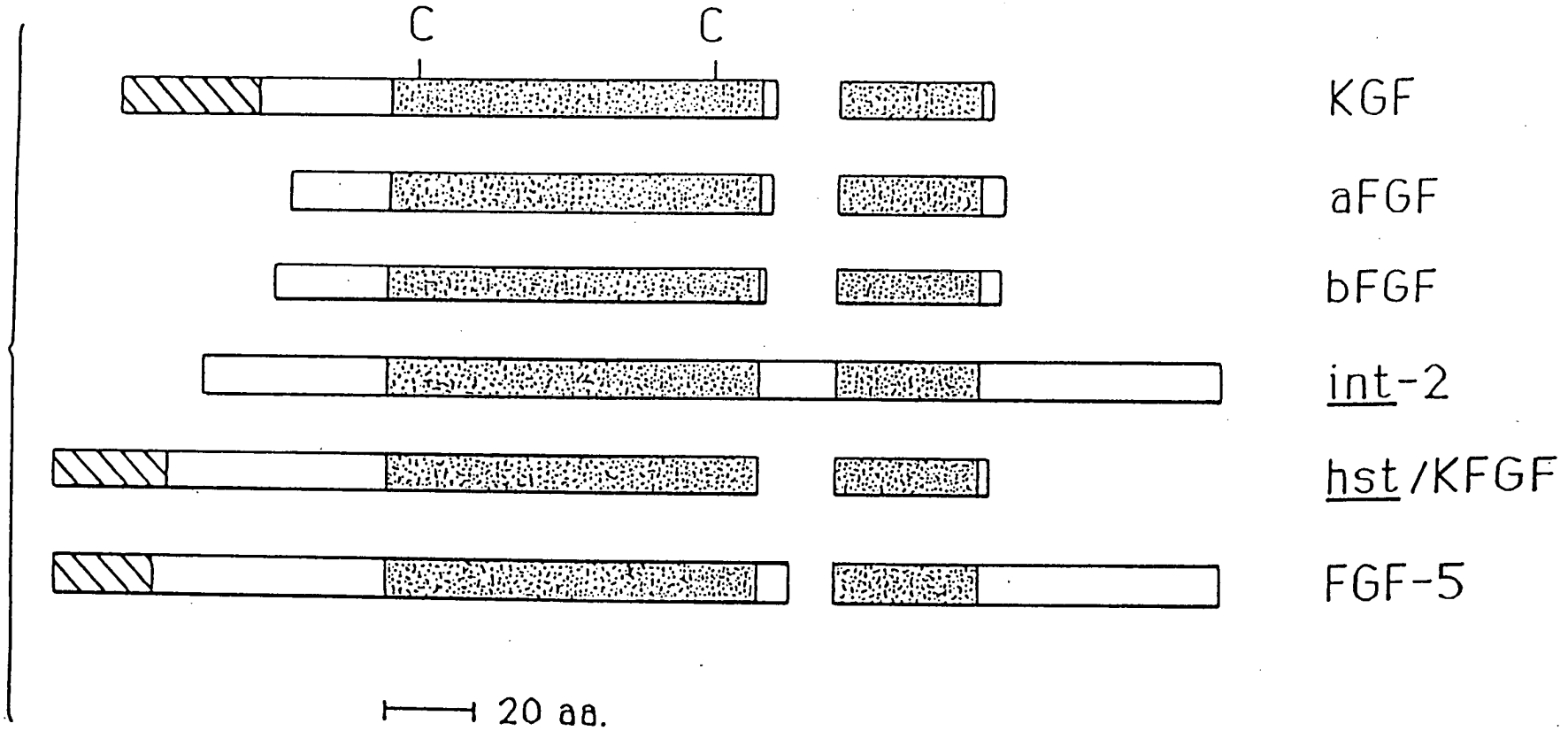
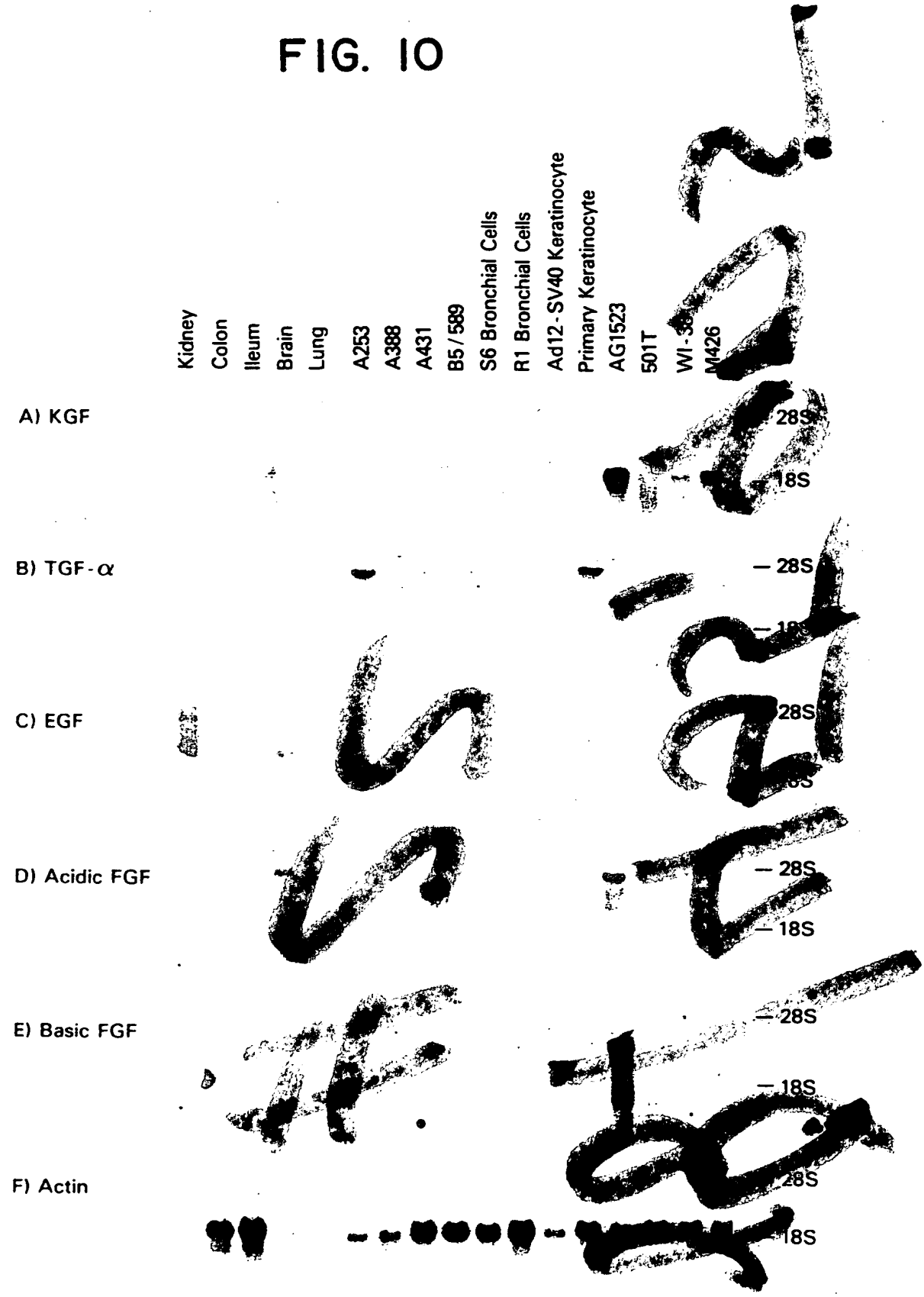


FIG. 10


Kidney
Colon
Ileum
Brain
Lung
A253
A388
A431
B5/589
S6 Bronchial Cells
R1 Bronchial Cells
Ad12-SV40 Keratinocyte
Primary Keratinocyte
AG1523
501T
WI-38
M426
A) KGF
B) TGF-α
C) EGF
D) Acidic FGF
E) Basic FGF
F) Actin
28S
18S